

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Eaton, Dan L.
DeSauvage, Frederic J.
- (ii) TITLE OF INVENTION: MPL LIGAND
- 10 (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)
- 25 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 4-APR-1994
(C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994
- 35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994
- 40 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994
- 45 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: 871P3
- 50 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/225-1249
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
1 5 10 15
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
20 25 30
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
35 40 45
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
50 55 60
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
65 70 75
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
80 85 90
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
95 100 105
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
110 115 120
Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
125 130 135
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
140 145 150
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
155 160 165
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
170 175 180
Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
185 190 195
Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
200 205 210

	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe
					215					220					225
5	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu
					230					235					240
	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn
					245					250					255
10	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly
					260					265					270
	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro
15					275					280					285
	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro
					290					295					300
20	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr
					305					310					315
	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro
					320					325					330
25	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His
					335					340					345
	Ser	Gln	Asn	Leu	Ser	Gln	Glu	Gly							
30					350			353							

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	TCTTCCTACC	CATCTGCTCC	CCAGAGGGCT	GCCTGCTGTG	CACTTGGGTC	50
45	CTGGAGCCCT	TCTCCACCCG	GATAGATTCC	TCACCCTTGG	CCCGCCTTTG	100
	CCCCACCCTA	CTCTGCCCAG	AAGTGCAAGA	GCCTAAGCCG	CCTCCATGGC	150
50	CCCAGGAAGG	ATTCAGGGGA	GAGGCCCCAA	ACAGGGAGCC	ACGCCAGCCA	200

GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
AGACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750
CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
TACCTGAACA GGATACACGA ACTCTTGAAT GGAATCGTG GACTCTTTCC 1000
TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050
CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100

CCAASCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150

5 CTTGCCCAAC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200

CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250

10 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300

15 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350

AACTGGACAA GATTTCTTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400

20 GGGATACACA GGAAGTAAAA GGAATCATT TTCTACTGTA CATTATAAAC 1450

CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500

25 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550

30 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600

GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650

35 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700

CATTCTCAGT GGAAGTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750

40 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795

45 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
1 5 10 15
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
20 25 30
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
35 40 42

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100
GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT COTGCTTG TG ACCTCCGAGT 150
CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200
GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250
CTCCCAGGAA GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT 300
TCTTCCCATA TTGTCCCCAC CTA CTGATCA CACTCTCTGA CAGAATTAT 350
TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTAAGGACC TTATGGTGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA 50
GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA 100
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA 150
GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT 200
CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT 250
GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA 300
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA 350
AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	
					35					40					45	
5	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	
					50					55					60	
	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	
					65					70					75	
10	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
					95					100					105	
15	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	
					110					115					120	
20	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	
					125					130					135	
	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	
					140					145					150	
25	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	
					155					160					165	
	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	
					170					175					180	
30	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	
					185					190					195	
	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly	
35					200					205					210	
	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr	
					215					220					225	
40	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe	
					230					235					240	
	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	
45					245					250					255	
	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	
					260					265					270	
50	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	
					275					280					285	

Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His
290 295 300

5 Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
320 325 330

10 Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1 5 10 15

25 Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
35 40 45

30 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60

35 Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90

40 Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120

45 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135

50 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
140 145 150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165

Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50
AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100
ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150
ATTGCTCCT GCGGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200
AGCCCCGTAG CTCCTGCCTG TGACCCCAAG CTCCTAAATA AACTGCTGCG 250
TGAATCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300
CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350
TGAAAAACC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400
GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450
CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500
TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550
CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACCTG CTTCGGGGAA 600

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AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG 650
 ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700
 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750
 TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800
 AGAGTCAAGA TTA~~CT~~CCTGG TCAGCTAAAT CAAACCTCCA GGCCCCAGT 850
 CCAAATCTCT GGATACCTGA ~~AG~~AGGACACA CGGACCTGTG AATGGA~~ACT~~C 900
 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950
 TCGCCCGGAG CTTTCAACAA AGGCTOCCTG GCATTCAACC TCCAGGGTGG 1000
 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC 1050
 CTTACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC 1100
 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150
 AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ~~AC~~ATAGCGCG 1200
 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250
 AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT 1300
 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG 1350
 GAGCTATTTT TTTTAACT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400
 TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT TCT 1443

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

10 Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
1 5 10 15
Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
20 25 30
15 Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
35 40 45
20 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
50 55 60
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
65 70 75
25 Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
80 85 90
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
95 100 105
30 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
110 115 120
35 Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu
125 130 135
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu
140 145 150
40 Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu
155 160 165
Val Glu Gly Pro Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr
170 175 180
45 Ala Val Pro Ser Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe
185 190 195
50 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr
200 205 210

	Ala	Arg	Thr	Ala	Gly	Pro	Gly	Leu	Leu	Ser	Arg	Leu	Gln	Gly	Phe
					215					220					225
5	Arg	Val	Lys	Ile	Thr	Pro	Gly	Gln	Leu	Asn	Gln	Thr	Ser	Arg	Ser
					230					235					240
	Pro	Val	Gln	Ile	Ser	Gly	Tyr	Leu	Asn	Arg	Thr	His	Gly	Pro	Val
					245					250					255
10	Asn	Gly	Thr	His	Gly	Leu	Phe	Ala	Gly	Thr	Ser	Leu	Gln	Thr	Leu
					260					265					270
	Glu	Ala	Ser	Asp	Ile	Ser	Pro	Gly	Ala	Phe	Asn	Lys	Gly	Ser	Leu
					275					280					285
15	Ala	Phe	Asn	Leu	Gln	Gly	Gly	Leu	Pro	Pro	Ser	Pro	Ser	Leu	Ala
					290					295					300
	Pro	Asp	Gly	His	Thr	Pro	Phe	Pro	Pro	Ser	Pro	Ala	Leu	Pro	Thr
					305					310					315
	Thr	His	Gly	Ser	Pro	Pro	Gln	Leu	His	Pro	Leu	Phe	Pro	Asp	Pro
					320					325					330
25	Ser	Thr	Thr	Met	Pro	Asn	Ser	Thr	Ala	Pro	His	Pro	Val	Thr	Met
					335					340					345
	Tyr	Pro	His	Pro	Arg	Asn	Leu	Ser	Gln	Glu	Thr				
					350					355	356				

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40	Ser	Pro	Val	Ala	Pro	Ala	Cys	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu
	1				5					10					15
	Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro
					20					25					30
45	Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp
					35					40					45
50	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Ser	Lys	Ala
					50					55					60

	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu	Leu	Leu	Glu	Gly	Val	Met
					65					70					75
5	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	Leu	Ser	Ser	Leu	Leu
					80					85					90
	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
					95					100					105
10	Gly	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro
					110					115					120
	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln	Leu	Leu	Arg	Gly	Lys	Val
					125					130					135
15	Arg	Phe	Leu	Leu	Leu	Val	Glu	Gly	Pro	Thr	Leu	Cys	Val	Arg	Arg
					140					145					150
	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser	Ser	Thr	Ser	Gln	Leu	Leu
					155					160					165
20	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr
					170					175					180
25	Asn	Phe	Ser	Val	Thr	Ala	Arg	Thr	Ala	Gly	Pro	Gly	Leu	Leu	Ser
					185					190					195
	Arg	Leu	Gln	Gly	Phe	Arg	Val	Lys	Ile	Thr	Pro	Gly	Gln	Leu	Asn
					200					205					210
30	Gln	Thr	Ser	Arg	Ser	Pro	Val	Gln	Ile	Ser	Gly	Tyr	Leu	Asn	Arg
					215					220					225
	Thr	His	Gly	Pro	Val	Asn	Gly	Thr	His	Gly	Leu	Phe	Ala	Gly	Thr
					230					235					240
35	Ser	Leu	Gln	Thr	Leu	Glu	Ala	Ser	Asp	Ile	Ser	Pro	Gly	Ala	Phe
					245					250					255
	Asn	Lys	Gly	Ser	Leu	Ala	Phe	Asn	Leu	Gln	Gly	Gly	Leu	Pro	Pro
					260					265					270
	Ser	Pro	Ser	Leu	Ala	Pro	Asp	Gly	His	Thr	Pro	Phe	Pro	Pro	Ser
					275					280					285
45	Pro	Ala	Leu	Pro	Thr	Thr	His	Gly	Ser	Pro	Pro	Gln	Leu	His	Pro
					290					295					300
	Leu	Phe	Pro	Asp	Pro	Ser	Thr	Thr	Met	Pro	Asn	Ser	Thr	Ala	Pro
					305					310					315

His Pro Val Thr Met Tyr Pro His Pro Arg Asn Leu Ser Gln Glu
320 325 330

Thr
331

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu
20 25 27

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCNGCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCGCGGCG GTCGGACACT GGGGGCTGAG GATTATTTG ACGGAGCACT 50

ACTGGTGCAA GTCGTGCCG 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTCGTGGAG GCCGTACACT GGGGGCTGAG GATTTATTTG ACGAAGCACT 50

GCTGGTGCAG GTAGTGCCG 69

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTCGTGGCG GCCGTACACT GGGGGCTGAG GATTTATTTG ACGAAGCACT 50

GCTAGTACAG ATAGTGCCA 69

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGTCTGCCG TGAAGGACAT GG 22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His
20 23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
1 5 10 15
Val Leu Leu Pro Ala Val Asp Phe
20 23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15
Asp Ile Leu Gly Ala Val Thr Leu
20 23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15
Cys Leu Ser Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
1 5 10 15
Gln Ser Leu
18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
1 5 10 15
Asp Pro Asn Ala Ile Phe
20 21

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15
Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25